

SEQUENCE LISTING

<110> Leo G.J. FRENKEN
Cornelis P.E. van der LOGT
Vin-Miin TEH
Martine E. VERHOEYEN
Joy E. WILKINSON
Stephen A. JOBLING

<120> Production of Antibodies

<130> PNK/060113/0275850 - T7060C

<140> US 09/737,476

<141> 2000-12-18

<150> EP 99310188.0

<151> 1999-12-17

<160> 67

<170> MS Word

<210> 1

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> VHH with peptide linker

<220>

<221> CDS

<222> (1)..(417)

<400> 1

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Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	
1				5					10					15		

tct	ctg	aga	ctc	tcc	tgt	gca	gcc	tgc	gga	cgc	gcc	acc	agt	ggc	cat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Ala	Thr	Ser	Gly	His	
			20					25					30			

ggc	cac	tat	ggc	atg	ggc	tgg	ttc	cgc	cag	gtt	cca	ggg	aag	gag	cgt	144
Gly	His	Tyr	Gly	Met	Gly	Trp	Phe	Arg	Gln	Val	Pro	Gly	Lys	Glu	Arg	
			35				40					45				

gag	ttt	gtc	gca	gct	att	agg	tgg	agt	ggc	aaa	gag	aca	tgg	tat	aaa	192
Glu	Phe	Val	Ala	Ala	Ile	Arg	Trp	Ser	Gly	Lys	Glu	Thr	Trp	Tyr	Lys	
			50			55					60					

093450000"9242260



gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc aag act 240
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
 65 70 75 80

acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg gcc gtt 288
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95

tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc ctg ccg 336
 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
 100 105 110

gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc tcc tca 384
 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 115 120 125

gaa caa aaa ctc atc tca gaa gag gat ctg aat taataagggc taagctcgaa 437
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 130 135

ttc 440

<210> 2

<211> 139

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<213> Artificial Sequence

<220>

<223> VHH with peptide linker

<400> 2

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His
 20 25 30

Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
 35 40 45

Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
 50 55 60

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
 65 70 75 80

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
 100 105 110

Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 115 120 125

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
130 135

<210> 3

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> myc linker

<400> 3

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
1 5 10

<210> 4

<211> 471

<212> DNA

<213> Artificial Sequence

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<223> VHH with linker

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<222> (1)..(459)

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Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

tct ctg aga ctc tcc tgt gta gct tct gaa agc agc ttc agc aac aat 96
Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
20 25 30

cac atg ggc tgg tac cgc cgg gct cca ggg aac cag cgc gag ctg gtc 144
His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
35 40 45

gca act att agt cct ggt ggt agc aca cac tat gta gac tcc gtg aag 192
Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
50 55 60

TOE080"924260

ggc cga ttc acc atc tcc cga gac aac gcc aag aac aca gtg tat cta	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu	
65 70 75 80	
caa atg gac agc ctg aaa cca gag gac acg gcc gtc tat tac tgt gct	288
Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
gcc aag ggg agg ggg ctg cag gct atg cag tac tgg ggc cag ggg acc	336
Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr	
100 105 110	
ctg gtc acc gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg	384
Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala	
115 120 125	
gcc gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc	432
Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile	
130 135 140	
tca gaa gag gat ctg aat ggg gcc gca tagtaacaat tg	471
Ser Glu Glu Asp Leu Asn Gly Ala Ala	
145 150	
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1 5 10 15	
Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn	
20 25 30	
His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val	
35 40 45	
Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys	
50 55 60	
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu	
65 70 75 80	
Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr	
100 105 110	

Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
115 120 125

Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
130 135 140

Ser Glu Glu Asp Leu Asn Gly Ala Ala
145 150

<210> 6

<211> 468

<212> DNA

<213> Artificial Sequence

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<223> VHH with linker

<220>

<221> CDS

<222> (1)..(456)

<400> 6

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

tct ctg aga ctc tcc tgt gta gcc tct gga aac acc ttc agt atc ata 96
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
20 25 30

gct atg gcc tgg tac cgc cag gct cca ggg aag cag cgc gag gtg gtc 144
Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
35 40 45

gca agt att aat agt att ggc agc aca aat tat gca gac tcc gtg aag 192
Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

ggg cga ttc acc atc tcc aga gac aac gcc aag aac aca gtg tat ctg 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

caa atg agc agc ctg aaa cct gag gac acg gcc gtc tat tac tgt gct 288
Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

gcc ggt aat ttg ctg gtt aag agg cct tac tgg ggc cag ggg acc ctg 336
Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
100 105 110

gtc acc gtc tcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc 384
Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
115 120 125

0973745-080301

gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca 432
Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
130 135 140

gaa gag gat ctg aat ggg gcc gca tagtaacaat tg 468
Glu Glu Asp Leu Asn Gly Ala Ala
145 150

<210> 7

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH with linker

<400> 7

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
20 25 30

Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
35 40 45

Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
115 120 125

Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
130 135 140

Glu Glu Asp Leu Asn Gly Ala Ala
145 150

<210> 8

<211> 462

<212> DNA

09737476-080301

0934E/60

<213> Artificial Sequence

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<223> VHH with linker

<220>

<221> CDS

<222> (1)..(450)

<400> 8

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1 5 10 15	
gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc	96
Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe	
20 25 30	
agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt	144
Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg	
35 40 45	
gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg	192
Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala	
50 55 60	
gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac	240
Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn	
65 70 75 80	
acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt	288
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val	
85 90 95	
tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc	336
Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr	
100 105 110	
gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat	384
Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His	
115 120 125	
cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag	432
His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu	
130 135 140	
gat ctg aat ggg gcc gca tagtaacaat tg	462
Asp Leu Asn Gly Ala Ala	
145 150	

<210> 9

<211> 150

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acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag	48
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1 5 10 15	
gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc	96
Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe	
20 25 30	
agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt	144
Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg	
35 40 45	
gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg	192
Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala	
50 55 60	
gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac	240
Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn	
65 70 75 80	
acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt	288
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val	
85 90 95	
tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc	336
Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr	
100 105 110	
gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat	384
Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His	
115 120 125	
cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag	432
His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu	
130 135 140	
gat ctg aat agt gag aaa gat gag cta tgataacaat tg	471
Asp Leu Asn Ser Glu Lys Asp Glu Leu	
145 150	

<210> 11

<211> 153

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH with linker

<400> 11

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20 25 30

Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
 35 40 45
 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
 50 55 60
 Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
 65 70 75 80
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110
 Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
 115 120 125
 His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 130 135 140
 Asp Leu Asn Ser Glu Lys Asp Glu Leu
 145 150

<210> 12

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 12

agctgcgatac gcaagcttgg taccgggaat tctctaga

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<210> 13

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 13

aatttctaga gaattcccgg taccaagctt gcttgcgatac gc

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<210> 14

<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic insert
<400> 14
tcgacccatg gcccgctagc caattggagc t 31

<210> 15
<211> 23
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<213> Artificial Sequence
<220>
<223> synthetic insert
<400> 15
ccaattggct agcgggcat ggg 23

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 16
ccacccacga gggaacatcg tg 22

<210> 17
<211> 39
<212> DNA
<213> Artificial Sequence
<220>
<223> primer

<400> 17
gaattcccat ggtttacact cgaggtcctc tccaaatga 39

<210> 18
<211> 189
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR product

<400> 18
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ggattgatgt gatatctcca ctgacgtaag ggatgacgca caatcccact atccttcgca 120
agacccttcc tttatataag gaagttcatt tcatttggag aggacctcga gtgtaaacca 180
tggaattc 189

<210> 19
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> sequencing primer

<400> 19
ccggcaacag gattcaatct t 21

<210> 20
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic insert

<400> 20
agctccatgg gattgttct cttttcacia ttgccttcat 40

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 <210> 25
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic insert
 <400> 25
 ggaaacagct atgaccatga ttac 24

 <210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic insert
 <400> 26
 tttcccagtc acgacgttgt 20

 <210> 27
 <211> 107
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic fragment encoding PRIa leader
 <220>
 <221> CDS
 <222> (3)..(104)

<400> 27

cc atg gga ttt gtt ctc ttt tca caa ttg cct tca ttt ctt ctt gtc 47
Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val
1 5 10 15

tct aca ctt ctc tta ttc cta gta ata tcc cac tct tgc cgt gcc cag 95
Ser Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Gln
20 25 30

gtg cag ctg cag 107
Val Gln Leu

<210> 28

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic fragment encoding PRIa leader

<400> 28

Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
1 5 10 15

Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Gln Val
20 25 30

Gln Leu

<210> 29

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 29

gacatcccat ggcaagcatc a 21

<210> 30

<211> 21

<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer

<400> 30

aagcttggtta acagccctta a

21

<210> 31

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 31

agggctgtta acaaacttga t

21

<210> 32

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 32

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44

<210> 33

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> sequencing primer

<400> 33

aattaaccct cactaaagg

19

<210> 34

<211> 254

<212> DNA

<213> Artificial Sequence

<220>

<223> GBSS leader

<220>

<221> CDS

<222> (3)..(254)

<400> 34

cc atg gca agc atc aca gct tca cac cac ttt gtg tca aga agc caa 47
Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln
1 5 10 15

act tca cta gac acc aaa tca acc ttg tca cag ata gga ctc agg aac 95
Thr Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn
20 25 30

cat act ctg act cac aat ggt tta agg gct gtt aac aaa ctt gat ggg 143
His Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly
35 40 45

ctc caa tca aga act aat act aag gta aca ccc aag atg gca tcc aga 191
Leu Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg
50 55 60

act gag acc aag aga cct gga tgc tca gct acc att gtt tgt gga aaa 239
Thr Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys
65 70 75

cag gtg cag ctg cag 254
Gln Val Gln Leu Gln
80

<210> 35

<211> 84

<212> PRT

<220>

<223> GBSS leader

<213> Artificial Sequence

<400> 35

Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln Thr
 1 5 10 15
 Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn His
 20 25 30
 Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly Leu
 35 40 45
 Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg Thr
 50 55 60
 Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys Gln
 65 70 75 80
 Val Gln Leu Gln

<210> 36

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 36

catgcaggtg cagctgca

18

<210> 37

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 37

gctgcacctg

10

<210> 38

<211> 24

<212> DNA

T0E080" 924260

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 38

cgcaagaccc ttctctata taag

24

<210> 39

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 39

gagctcgaat tcttattata gctcatcttt ctctgaattc agatcctctt ctgagatgag

60

<210> 40

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 40

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
20 25

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 41

atcctcaact tccaatcaga

20

<210> 42

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 42

ttcttgagag atagcttga

19

<210> 43

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 43

gatcccatgg cccgctagcc aattggagct

30

<210> 44

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 44

ccaattggct agcgggccat gg

22

<210> 45

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 45

gatccacctc gagtgtaaac catggcccg

29

<210> 46

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 46

ctagcgggcc atggtttaca ctcgaggtg

29

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 47

attgcctacg gcagccgctg

20

<210> 48

<211> 51

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

<400> 48

tccaaccaat tggtactatg cgccccatt cagatcctct tctgagatga g

51

<220>

<223> PCR primer

<400> 52

cgttttcgtc ggtaatcacc attcc 25

<210> 53

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> sequencing primer

<400> 53

cgcaagaccc ttcctttata taag 24

<210> 54

<211> 1154

<212> DNA

<213> Artificial Sequence

<220>

<223> HCV33-hinge-CH2-CH3

<220>

<221> CDS

<222> (3)..(1136)

<400> 54

cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct 47
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
1 5 10 15

ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt 95
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser
20 25 30

ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag 143
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys
35 40 45

gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg 191
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp
50 55 60

tat	aaa	gac	tcc	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gat	aac	gcc	239
Tyr	Lys	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	
	65					70					75					
aag	act	acg	gtt	tat	ctg	caa	atg	aac	agc	ctg	aaa	cct	gaa	gat	acg	287
Lys	Thr	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	
	80				85					90					95	
gcc	gtt	tat	tat	tgt	gcc	gct	cga	ccg	gtc	cgc	gtg	gat	gat	att	tcc	335
Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Pro	Val	Arg	Val	Asp	Asp	Ile	Ser	
				100					105					110		
ctg	ccg	gtt	ggg	ttt	gac	tac	tgg	ggc	cag	ggg	acc	cag	gtc	acc	gtc	383
Leu	Pro	Val	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	
			115					120					125			
tcc	tca	gaa	ccc	aag	aca	cca	aaa	cca	caa	cca	caa	cca	caa	cca	caa	431
Ser	Ser	Glu	Pro	Lys	Thr	Pro	Lys	Pro	Gln	Pro	Gln	Pro	Gln	Pro	Gln	
		130					135					140				
cca	caa	ccc	aat	cct	aca	aca	gaa	tcc	aag	tgt	ccc	aaa	tgt	cca	gcc	479
Pro	Gln	Pro	Asn	Pro	Thr	Thr	Glu	Ser	Lys	Cys	Pro	Lys	Cys	Pro	Ala	
		145				150					155					
cct	gag	ctc	ctg	gga	ggg	ccc	tca	gtc	ttc	atc	ttc	ccc	ccg	aaa	ccc	527
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	
	160				165					170					175	
aag	gac	gtc	ctc	tcc	att	tct	ggg	agg	ccc	gag	gtc	acg	tgc	gtt	gtg	575
Lys	Asp	Val	Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	
				180					185					190		
gta	gac	gtg	ggc	cag	gaa	gac	ccc	gag	gtc	agt	ttc	aac	tgg	tac	att	623
Val	Asp	Val	Gly	Gln	Glu	Asp	Pro	Glu	Val	Ser	Phe	Asn	Trp	Tyr	Ile	
			195					200					205			
gat	ggc	gca	gag	gtg	cga	acg	gcc	aac	acg	agg	cca	aaa	gag	gaa	cag	671
Asp	Gly	Ala	Glu	Val	Arg	Thr	Ala	Asn	Thr	Arg	Pro	Lys	Glu	Glu	Gln	
		210					215					220				
ttc	aac	agc	acg	tac	cgc	gtg	gtc	agc	gtc	ctg	ccc	atc	cag	cac	cag	719
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	
	225					230					235					
gac	tgg	ctg	acg	ggg	aaa	gag	ttc	aaa	tgc	aag	gtc	aac	aac	aaa	gct	767
Asp	Trp	Leu	Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	
	240				245					250					255	
ctc	ccg	gcc	ccc	atc	gag	aag	acc	atc	tcc	aag	gcc	aaa	ggg	cag	acc	815
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	
				260					265					270		
cgg	gag	ccg	cag	gtg	tac	gcc	ctg	gcc	cca	cac	cgg	gaa	gag	ctg	gcc	863
Arg	Glu	Pro	Gln	Val	Tyr	Ala	Leu	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	
			275				280						285			
aag	gac	acc	gtg	agc	gta	acc	tgc	ctg	gtc	aaa	ggc	ttc	tac	cca	cct	911
Lys	Asp	Thr	Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Pro	
		290					295					300				

gat atc aac gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc 959
 Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly
 305 310 315

acc tac gcc acc acg cca ccc cag ctg gac aac gac ggg acc tac ttc 1007
 Thr Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe
 320 325 330 335

ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag cgg gga gaa 1055
 Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu
 340 345 350

acc ttc acc tgt gtg gtg atg cac gag gcc ctg cac aac cac tac acc 1103
 Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr
 355 360 365

cag aaa tcc atc acc cag tct tcg ggt aaa taa taagaattcg agctcgaa 1154
 Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
 370 375

<210> 55

<211> 377

<212> PRT

<213> Artificial Sequence

<220>

<223> HCV33-hinge-CH2-CH3

<400> 55

Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
 1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly
 20 25 30

His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu
 35 40 45

Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr
 50 55 60

Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
 65 70 75 80

Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
 85 90 95

Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu
 100 105 110

Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125

Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln Pro
 130 135 140
 Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro
 145 150 155 160
 Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 165 170 175
 Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val
 180 185 190
 Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp
 195 200 205
 Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe
 210 215 220
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp
 225 230 235 240
 Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu
 245 250 255
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg
 260 265 270
 Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala Lys
 275 280 285
 Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp
 290 295 300
 Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr
 305 310 315 320
 Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu
 325 330 335
 Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr
 340 345 350
 Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 355 360 365
 Lys Ser Ile Thr Gln Ser Ser Gly Lys
 370 375

<210> 56

<211> 1172

<212> DNA

<213> Artificial Sequence

<220>

<223> hinge-HCV33-CH2-CH3-SEKDEL

<220>

<221> CDS

<222> (3)..(1154)

<400> 56

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1 5 10 15	
ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt	95
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser	
20 25 30	
ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag	143
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys	
35 40 45	
gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg	191
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp	
50 55 60	
tat aaa gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc	239
Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala	
65 70 75	
aag act acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg	287
Lys Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr	
80 85 90 95	
gcc gtt tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc	335
Ala Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser	
100 105 110	
ctg ccg gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc	383
Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val	
115 120 125	
tcc tca gaa ccc aag aca cca aaa cca caa cca caa cca caa cca caa	431
Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln	
130 135 140	
cca caa ccc aat cct aca aca gaa tcc aag tgt ccc aaa tgt cca gcc	479
Pro Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala	
145 150 155	
cct gag ctc ctg gga ggg ccc tca gtc ttc atc ttc ccc ccg aaa ccc	527
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro	
160 165 170 175	
aag gac gtc ctc tcc att tct ggg agg ccc gag gtc acg tgc gtt gtg	575
Lys Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val	
180 185 190	
gta gac gtg ggc cag gaa gac ccc gag gtc agt ttc aac tgg tac att	623
Val Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile	
195 200 205	

gat ggc gca gag gtg cga acg gcc aac acg agg cca aaa gag gaa cag Asp Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln 210 215 220	671
ttc aac agc acg tac cgc gtg gtc agc gtc ctg ccc atc cag cac cag Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln 225 230 235	719
gac tgg ctg acg ggg aaa gag ttc aaa tgc aag gtc aac aac aaa gct Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala 240 245 250 255	767
ctc ccg gcc ccc atc gag aag acc atc tcc aag gcc aaa ggg cag acc Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr 260 265 270	815
cgg gag ccg cag gtg tac gcc ctg gcc cca cac cgg gaa gag ctg gcc Arg Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala 275 280 285	863
aag gac acc gtg agc gta acc tgc ctg gtc aaa ggc ttc tac cca cct Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro 290 295 300	911
gat atc aac gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly 305 310 315	959
acc tac gcc acc acg cca ccc cag ctg gac aac gac ggg acc tac ttc Thr Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe 320 325 330 335	1007
ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag cgg gga gaa Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu 340 345 350	1055
acc ttc acc tgt gtg gtg atg cac gag gcc ctg cac aac cac tac acc Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr 355 360 365	1103
cag aaa tcc atc acc cag tct tcg ggt aaa tct gag aaa gat gag cta Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys Ser Glu Lys Asp Glu Leu 370 375 380	1151
taa taagaattcg agctcgaa	1172

<210> 57

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> hinge-HCV33-CH2-CH3-SEKDEL

<400> 57

09737476-080301

Met	Glu	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	
1				5					10					15		
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Ala	Thr	Ser	Gly	
			20					25					30			
His	Gly	His	Tyr	Gly	Met	Gly	Trp	Phe	Arg	Gln	Val	Pro	Gly	Lys	Glu	
		35					40					45				
Arg	Glu	Phe	Val	Ala	Ala	Ile	Arg	Trp	Ser	Gly	Lys	Glu	Thr	Trp	Tyr	
		50				55					60					
Lys	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	
65					70					75					80	
Thr	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	
				85					90					95		
Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Pro	Val	Arg	Val	Asp	Asp	Ile	Ser	Leu	
			100					105					110			
Pro	Val	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	
		115					120					125				
Ser	Glu	Pro	Lys	Thr	Pro	Lys	Pro	Gln	Pro	Gln	Pro	Gln	Pro	Gln	Pro	
	130					135					140					
Gln	Pro	Asn	Pro	Thr	Thr	Glu	Ser	Lys	Cys	Pro	Lys	Cys	Pro	Ala	Pro	
					150					155					160	
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	
				165					170					175		
Asp	Val	Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	
			180					185					190			
Asp	Val	Gly	Gln	Glu	Asp	Pro	Glu	Val	Ser	Phe	Asn	Trp	Tyr	Ile	Asp	
		195				200						205				
Gly	Ala	Glu	Val	Arg	Thr	Ala	Asn	Thr	Arg	Pro	Lys	Glu	Glu	Gln	Phe	
	210					215					220					
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	
	225				230					235					240	
Trp	Leu	Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	
				245					250					255		
Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	
			260					265					270			
Glu	Pro	Gln	Val	Tyr	Ala	Leu	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	Lys	
		275					280					285				
Asp	Thr	Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Pro	Asp	
		290				295					300					
Ile	Asn	Val	Glu	Trp	Gln	Arg	Asn	Gly	Gln	Pro	Glu	Ser	Glu	Gly	Thr	
305					310					315					320	

Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu
 325 330 335

Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr
 340 345 350

Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 355 360 365

Lys Ser Ile Thr Gln Ser Ser Gly Lys Ser Glu Lys Asp Glu Leu
 370 375 380

<210> 58

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 58

aggggaccca ggtcacccgtc tcctcagaac c

31

<210> 59

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 59

gagctttggtt gttgaccttg catttgaact ctttccc

37

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 60

097374-080301

caaagtcaag gtcaacaaca aagctc

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 61

ttcgagctcg aattcttatt atttaccoga agactgggtg at

42

<210> 62

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> sequencing primer

<400> 62

ctgaggagac ggtgacctgg gtcccct

27

<210> 63

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 63

agcccctgag ctctgggag ggccctcagt cttcatcttc cccccg

46

<210> 64

<211> 61

<212> DNA

<213> Artificial Sequence

09737476 "080301"

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<220>
<223> PCR primer
<400> 64
ttcgagctcg aattcttatt atttaccga agactgggtg atggatttct gggtagtg 60
g 61

<210> 65
<211> 79
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 65
ttcgagctcg aattcttatt atagctcatc tttctcagat ttaccgaag actgggtgat 60
ggatttctgg gtgtagtg 79

<210> 66
<211> 461
<212> DNA
<213> Artificial Sequence
<220>
<223> VHH with linker
<220>
<221> CDS
<222> (3)..(449)
<400> 66
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Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15
gct ggg ggg tct ctg agg ctc tcc tgt gca gcc tct gga agc att ttc 95
Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe
20 25 30

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aga cgt ccg cat atg ggt tgg ttc cgc cag gct cca ggg cag gag cgc 143
 Arg Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg
 35 40 45

gag ttg gtc gca ctg att tct gcg ggt ggt cgt aca tgg tat gca gac 191
 Glu Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp
 50 55 60

tcc gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg 239
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
 65 70 75

ctg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt tat 287
 Leu Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr
 80 85 90 95

tac tgt act gcc ggg ggt tct tac tgg ggc cag ggg acc cag gtc acc 335
 Tyr Cys Thr Ala Gly Gly Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110

gtc gcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc gcc cat 383
 Val Ala Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala Ala His
 115 120 125

cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag 431
 His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 130 135 140

gat ctg aat ggg gcc gca tagtaacaat tg 461
 Asp Leu Asn Gly Ala Ala
 145

<210> 67

<211> 149

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH with linker

<400> 67

Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
 1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Arg
 20 25 30

Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg Glu
 35 40 45

Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp Ser
 50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu
 65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Thr Ala Gly Gly Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
100 105 110

Ala Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala Ala His His
115 120 125

His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp
130 135 140

Leu Asn Gly Ala Ala
145

09737476-080304